## SEQUENCE LISTING

SEGOLIOE FIGURA															
<110>	Yaman	ouch	i Ph	arma	ceut	ical	Co.	, Lt	d.						
<120>	Screening method of agents for increasing insulin content														
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<220> <221> <222>		(100	08)									,			
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ctc at Leu II	c att e lle	gct Ala 20	act Thr	aac Asn	aca Thr	cta Leu	gtg Val 25	gct Ala	gtg Val	gct Ala	gtg Val	ctg Leu 30	ctg Leu	ttg Leu	96
atc ca lle Hi	s Lys 35	aat Asn	gat Asp	ggt Gly	gtc Val	agt Ser 40	ctc Leu	tgc Cys	ttc Phe	acc Thr	ttg Leu 45	aat Asn	ctg Leu	gct Ala	144
	et gac la Asp 50	acc Thr	ttg Leu	att He	ggt Gly 55	gtg Val	gcc Ala	atc lle	tct Ser	ggc Gly 60	cta Leu	ctc Leu	aca Thr	gac Asp	192
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GIn 65	Leu	Ser	Ser	Pro	Ser 70	Arg	Pro	Thr	Gln	Lys 75	Thr	Leu	Cys	Ser	Leu 80	
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atg Met	ctg Leu	atc Ile	acc Thr 100	ttt Phe	gac Asp	agg Arg	tac Tyr	ctt Leu 105	gcc Ala	atc !le	aag Lys	cag Gln	ccc Pro 110	ttc Phe	cgc Arg	336
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										gac Asp						576
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gct Ala	gga Gly 210	Gly	tat Tyr	cga Arg	tcc Ser	cca Pro 215	cgg Arg	act Thr	ccc Pro	agc Ser	gac Asp 220	Phe	aaa Lys	gct Ala	ctc Leu	672
cgt Arg 225	Thr	gtg Val	tct Ser	gtt Val	ctc Leu 230	He	ggg Gly	agc Ser	ttt Phe	gct Ala 235	Leu	tcc Ser	tgg Trp	acc Thr	ccc Pro 240	720
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Tyr Leu Val	ctg ( Leu ( 260													816
ctg ctc aac Leu Leu Asn 275														864
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	His	Pro	His	Phe 165	Val	Leu	Thr	Leu	Ser 170	Cys	Val	Gly	Phe	Phe 175	Pro
Ala	Met	Leu	Leu 180	Phe	Val	Phe	Phe	Tyr 185	Cys	Asp	Met	Leu	Lys 190	He	Ala
		195			Gln		200					205			
Ala	Gly 210	Gly	Tyr	Arg	Ser	Pro 215	Arg	Thr	Pro	Ser	Asp 220	Phe	Lys	Ala	Leu
Arg 225	Thr	Val	Ser	Val	Leu 230	He	Gly	Ser	Phe	Ala 235	Leu	Ser	Trp	Thr	Pro 240
Phe	Leu	lle	Thr	Gly 245	lle	Val	Gln	Val	Ala 250		GIn	Glu	Cys	His 255	Leu
Tyr	Leu	Va <sup>′</sup> l	Leu 260	Glu	Arg	Tyr	Leu	Trp 265	Leu	Leu	Gly	Val	Gly 270	Asn	Ser
Leu	Leu	Asn 275	Pro	Leu	lle	Tyr	Ala 280	Tyr	Trp	Gln	Lys	Glu 285	Val	Arg	Leu
Gln	Leu 290	Tyr	His	Met	Ala	Leu 295	Gly	Val	Lys	Lys	Val 300	Leu	Thr	Ser	Phe
Leu 305		Phe	Leu	Ser	Ala 310	Arg	Asn		Gly	Pro 315	Glu	Arg	Pro	Arg	G1u 320
Ser	Ser	Cys	His	11e 325	Val	Thr	He	Ser	Ser 330	Ser	Glu	Phe	Asp	Gly 335	
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5
10
15

ctt atc att gct gtt aat gcg ctg gtg gtt gtg gct atg ctg cta tca 96 Leu lie lie Ala Val Asn Ala Leu Val Val Val Ala Met Leu Leu Ser 20 25 30

atc tac aag aat gat ggt gtt ggc ctt tgc ttc acc tta aat ctg gcc 144 ile Tyr Lys Asn Asp Gly Val Gly Leu Cys Phe Thr Leu Asn Leu Ala

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cag Gln 65	ctc Leu	tcc Ser	agc Ser	tct Ser	gct Ala 70	cag Gln	cac His	aca Thr	cag Gln	aag Lys 75	acc Thr	ttg <sup>.</sup> Leu	tgt Cys	agc Ser	ctt Leu 80	240
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atg Met	ctg Leu	att lle	gcc Ala 100	ttt Phe	gac Asp	agg Arg	tac Tyr	ctg Leu 105	gcc Ala	att ile	aag Lys	cag Gln	ccc Pro 110	ctc Leu	cgt Arg	336
tac Tyr	ttc Phe	cag GIn 115	atc lle	atg Met	aat Asn	ggg Gly	ctt Leu 120	gta Val	gcc Ala	gga Gly	gga Gly	tgc Cys 125	att Ile	gca Ala	ggg Gly	384
ctg Leu	tgg Trp 130	ttg Leu	ata Ile	tct Ser	tac Tyr	ctt Leu 135	atc Ile	ggc Gly	ttc Phe	ctc Leu	cca Pro 140	ctt Leu	gga Gly	gtc Val	tcc Ser	432
ata Ile 145	ttc Phe	cag Gln	cag Gln	acc Thr	acc Thr 150	tac Tyr	cat His	ggg Gly	ccc Pro	tgc Cys 155	acc Thr	ttc Phe	ttt Phe	gct Ala	gtg Val 160	480
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gct Ala	gtg Val	ctc Leu	ctc Leu 180	ttt Phe	gtc Val	ttc Phe	ttc Phe	tac Tyr 185	tgt Cys	gac Asp	atg Met	ctc Leu	aag Lys 190	att Ile	gcc Ala	576
tct Ser	gtg Val	cac His 195	Ser	cag GIn	cac His	atc Ile	cgg Arg 200	aag Lys	atg Met	gaa Glu	cat His	gca Ala 205	gga Gly	gcc Ala	atg Met	624
gtt Val	gga Gly 210	gct Ala	tgc Cys	cgg Arg	ccc Pro	cca Pro 215	Arg	cct Pro	gtc Val	aat Asn	gac Asp 220	Phe	aag Lys	gct Ala	gtc Val	672

1	ogg Arg 225	act Thr	gta Val	tct Ser	gtc Val	ctt Leu 230	att Ile	ggg Gly	agc Ser	ttc Phe	acc Thr 235	ctg Leu	tcc Ser	tgg Trp	tct Ser	ccg Pro 240	720
					agc Ser 245												768
	tac Tyr	caa GIn	gtg Val	ctg Leu 260	gaa Glu	aaa Lys	tac Tyr	ctc Leu	tgg Trp 265	ctc Leu	ctt Leu	gga Gly	gtt Val	ggc Gly 270	aac Asn	tcc Ser	816
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	cag Gln	ctc Leu 290	tgc Cys	cac His	atg Met	gcc Ala	ctg Leu 295	ggg Gly	gtg Val	aag Lys	aag Lys	ttc Phe 300	ttt Phe	act Thr	tca Ser	atc lle	912
					tcg Ser												960
	agc Ser	tcc Ser	tat Tyr	cac His	atc Ile 325	gtc Val	act Thr	atc Ile	agc Ser	cag Gln 330	ccg Pro	gag Glu	ctc Leu	gat Asp	ggc Gly 335	tag	1008
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				20					25					30			
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	Val	Ala 50	Asp		Leu	lle	Gly 55		Ala	lle	Ser	Gly 60		Val	Thr	Asp	
		Leu		Ser	Ser	Ala 70	Gln		Thr	Gln	Lys 75		Leu	Cys	Ser	Leu 80	
	65 Arg		Ala	Phe	· Val			Ser	Ala	Ala			Val	Leu	Thr		

				85					90					95	
		lle	100					105					110		
Tyr	Phe	GIn 115	He	Met	Asn	Gly	Leu 120	Val	Ala	Gly	Gly	Cys 125	He	Ala	Gly
Leu	Trp 130	Leu	He	Ser	Tyr	Leu 135	He	Gly	Phe	Leu	Pro 140	Leu	Gly	Val	Ser
145	Phe	GIn			150					155					160
Phe	His	Pro	Arg	Phe 165	Val	Leu	Thr	Leu	Ser 170	Cys	Ala	Gly	Phe	Phe 175	Pro
Ala	Val	Leu	Leu 180	Phe	Val	Phe	Phe	Tyr 185	Cys	Asp	Met	Leu	Lys 190	lle	Ala
Ser	Val	His 195	Ser	Gln	His	lle	Arg 200	Lys	Met	Glu	His	Ala 205	Gly	Ala	Met
Val	Gly 210	Ala	Cys	Arg	Pro	Pro 215	Arg	Pro	Val	Asn	Asp 220	Phe	Lys	Ala	Val
225		Val			230					235					240
Phe		He		245					250					255	
	•	Val	260					265					270		
		275					280					285			Gln
Gin	Leu 290	Cys	His	Met	Ala	Leu 295		Val	Lys	Lys	Phe 300	Phe	Thr	Ser	lle
Phe 305	Leu		Leu	Ser	Ala 310		Asn	Arg	Gly	Pro 315	Gln	Arg	Thr	Arg	Glu 320
Ser	Ser	Tyr	His	11e 325		Thr	He	Ser	GIn 330	Pro	Glu	Leu	Asp	Gly 335	

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<211> 28

<212> DNA

<213> Artificial Sequence

<220>

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<213>	Arti	ficial Sequ	ienće				
<220>							A STORY
	Desc	ription of	Artificial	Sequence: a	an artificia	ally synthe	esized
(220)		er sequence					
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	•	tottotaata	0050				24
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cacagac	cca	gcaccaggga	aatggtccgg	aaattgcagc	ctcagccccc	agccatctgo	240
cgaccc	ccc	accccaggcc	ctaatgggcc	aggcggcagg	ggttgacagg	taggggagat	300
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gcatcag	gaag	aggccat					377